

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 26, 2002, 06:09:02 ; Search time 24.91 seconds  
(without alignments)

667.127 Million cell updates/sec

Title: US-09-701-121-2

Perfect score: 649

Sequence: 1 PLATROGKPKSNLKARSR.....ANNVYKQYEDMVVESEGR 119

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 7407290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_1101.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	649	100.0	119	21	AAV44296	Mutant human MP52
2	645	99.4	119	17	AAW06920	Human MP52 growth
3	645	99.4	119	18	AAW19846	Human bone induction
4	645	99.4	120	16	AAW78731	Murine protein MP5
5	645	99.4	120	18	AAW26590	Human MP52 protein
6	645	99.4	120	14	AAW40800	TGF-beta-like clone
7	645	99.4	471	16	AAW69600	New TGF-beta fami
8	645	99.4	501	12	AAW36100	Human MP52 Homo
9	645	99.4	501	18	AAW19210	Human TGF-beta pro
10	645	99.4	501	18	AAW11900	Human high mol. wt
11	645	99.4	501	18	AAW01799	Human MP52 protein

12	645	99.4	501	18	AAW12770	Human bone morphol
13	645	99.4	501	19	AAW44868	TGF-beta super fami
14	645	99.4	501	19	AAW44008	Human MP52 Homo
15	645	99.4	501	22	AAW70529	Human TGF-beta MP5
16	640	98.6	495	15	AAW60022	Growth diff. regul
17	640	98.6	495	22	AAW84550	Amino acid sequen
18	639	98.5	119	21	AAW70752	Wild type mature b
19	639	98.5	119	21	AAW70756	Methionine oxidase
20	639	98.5	119	21	AAW70757	Protophane alkylat
21	639	98.5	119	21	AAW70758	Tryptophan alkylsu
22	639	98.5	501	17	AAW95635	Cartilage-derived
23	639	98.5	501	21	AAW92034	Human growth diff
24	559	86.1	102	21	AAW09554	Human BMP-1/GDF-5
25	559	86.1	102	21	AAW02819	Human BMP-1/GDF-5
26	559	86.1	102	21	AAW92578	BMP-1/GDF-5 finge
27	543	83.7	134	16	AAW66867	GDF-6, Mus sp. A
28	543	83.7	134	21	AAW12986	Murine growth diff
29	543	83.7	263	16	AAW78739	Murine m22 protein
30	543	83.7	263	18	AAW26595	Murine BMP-1 homo
31	540	83.2	421	16	AAW78730	Human mature VI-1
32	540	83.2	421	18	AAW26591	Human bone morphol
33	528	81.4	436	17	AAW95636	Cartilage derived
34	510	78.6	102	21	AAW09555	Murine GDF-6, SHG
35	510	78.6	102	21	AAW02821	Mouse GDF-6 amino
36	510	78.6	102	21	AAW92580	GDF-6 finger-1 hee
37	507	78.1	102	21	AAW09554	Human BMP-2/GDF-6
38	507	78.1	102	21	AAW02820	Human BMP-2/GDF-6
39	507	78.1	102	21	AAW92579	BMP-2/GDF-6 finge
40	495	76.3	102	21	AAW09556	Bovine BMP-2, SE
41	495	76.3	102	21	AAW02822	Bovine BMP-2 amin
42	495	76.3	102	21	AAW92581	BMP-2 finger-1 he
43	494	76.1	129	19	AAW54067	Bone morphogenetic
44	494	76.1	294	16	AAW78729	Human bone morphol
45	494	76.1	294	18	AAW44589	Human bone morphol

#### ALIGNMENTS

RESULT 1	
AAV44296	
ID	AAV44296 standard; Protein: 119 AA.
XX	
AC	AAV44296;
XX	
XX	29-FEB-2000 (first entry)
DI	
XX	
DE	Mutant human MP52 monomer protein.
XX	
XX	Mutant MP52 monomer protein; transforming growth factor-beta; TGF-beta;
KW	pKOT279 expression vector; osteocyte; bone morphogenetic; osteopathic;
KW	anti-arthritis activity; cartilage; osteoporosis; osteoarthritis;
KW	arthroosteilis; fracture; achondroplasia; dyschondrogenesis;
KW	achondrogenesis; palatoschisis; dysosteoconosis.
XX	
XX	Homo sapiens.
OS	Synthetic.
XX	
XX	
EH	Key Location/Qualifiers
FT	Misc-difference 83
FT	/note "Wild-type Cys replaced by Ala"
XX	
XX	W09961611-AL.
XX	
XX	02-DEC-1999.
XX	
XX	14-MAY-1999; 99W01H00866.
XX	
XX	22-MAY-1998; 98JP-0141379.
PR	
PA	(HMR1) HEPATH1 MAKUON ROUSSEL LTD.
XX	
PI	Kawai S., Kimura M., Muraki Y., Katsunaga M.

	FT	dimer	is used for treatment of bone, cartilage and dental disorders.
	XX	PP	
	PS		
	XX	claim 1;	Pages D6 19; 43pp; Japanese.
	CC	The present sequence is residues 484 to 601 of the human MP <sup>α</sup> /growth factor, a dimer of which can be used to treat bone, cartilage and dental disorders, including fractures, bone loss and periodontal disease. The dimer was prepared by transfection a host (preferably E. coli) with a suitable (plasmid) expression vector containing DNA encoding the monomer. The host was cultured, and inclusion bodies from the cells worked up to give the monomer, which was then converted into the dimer. The product was mixed with type I pig tendon collagen and injected into the large third web of 1CR mice. After 20 days 4 of 4 mice injected with 10 microg of the dimer showed bone/cartilage calcification around the injection site, compared to none in 0 of 4 mice treated with collagen only.	
	XX		
	SQ	Sequence	119 AA;
		Query Match:	99.4%; Score 645; DB 17; Length 119;
		Best Local Similarity	99.2%; Prod. No. 1c-59;
		Matches 118;	Conservative 0; Mismatches 1; Indels 0; Gaps
	QY	1	PLATICEKPPSKNKKAKCSKAHIVNIKKMGWOWIATLVEFAVDFECLFEFLRSKSLR 60 
	Dd	1	platicekppsknkkakcskaahivnikmgwowiatlvefavdfefclfe flrskslr 60 
	QY	61	PINIAVAQTILNNSEDESTPACTCPETSPISLTLDSSANNVVTKGVHMVVISGGR 119 
	Dd	61	piniavagtlnnnsedestpac tpetspisl tldssannvvtkgvdmvvisgr 119 
	RESULT 4		
	AAM19846		
	ID	AAM19846 standard;	Protein; 119 AA.
	XX		
	XX	AAM19846;	
	DD	12 FEB 1998	(first entry)
	DE	Human bone inducing factor	MP <sup>α</sup> /2.
	KW	Human; Bone inducing factor;	MP <sup>α</sup> /2; collagen; fracture;
	KX	polyoxyethylene-polyoxypylene glycol.	
	OS	Homo sapiens.	
	PN	Wo9718829 A1.	
	XX	29 MAY 1997.	
	XX	14 NOV 1996;	96WOJ100433A.
	XX	17 NOV 1995;	95JP 042240Z.
	PR	(FAMI ) BONE-TST JAPAN LTD.	
	PA	(FAMI ) BONE-TST PHARM & CHEM KK.	
	F1	Shimizu K., Tokyoama S;	
	XX		
	DR	WP1; 1997 01024 v/2B.	
	N	USBR; AM10296.	
	F1	Material for repairing bone and collagen, especially bone fracture or loss, comprising bone inducing factor and polyoxyethylene-polyoxypylene glycol compounds	
	XX	Example 4; Page 16, 17;	43pp; Japanese.
	PS	Bone and collagen inducing material has been developed which comprises bone inducing factor and polyoxyethylene-polyoxypylene glycol	

CC compounds. The present sequence represents human bone inducing factor  
 CC MP52. This material allows treatment without surgery. It is highly  
 CC absorbable because a carrier is used with the bone inducing factor.  
 CC and undergoes reversible sol-gel transition depending on the  
 CC temperature.

XX Sequence 119 AA;

Query Match 99.4%; Score 645; DB 18; Length 119;

Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATKCKKPSKKNLKARSKKALHVNFKMGWDGWIAPLEYAFBCEGLCEPPLKSHLE 60  
 II  
 DB 1 platrqrkpsknlkarskalkhntkdmqwdwllapleyatheaqlcetpirshle 60  
 QY 61 PINHAVIQLMNSMDPESTPTACVPTRLSPISILFIDSANNVVKQYEDMVVSESGTR 119  
 III  
 DB 61 ptnhaviqlmnsmdpestptceptrlspisilfidsannvvykqyedmvseseqr 119

RESULT 4

AAK78741  
 ID AAK78741 standard; Protein: 120 AA.

XX AAK78741:

XX 23-NOV-1995 (first entry)

XX Murine protein MP52.

XX Bone morphogenetic protein; MP52; tendon; ligament.

XX Mus musculus.

XX W09516045-A.

XX 15-JUN-1995.

XX 06-DEC-1994; 94MO-US14040.

XX 02-NOV-1994; 94US-0334576.

XX 07-DEC-1994; 94US-0164103.

XX 25-MAR-1994; 94US-0217780.

XX (GEMMY ) GENETICS INST INC.

XX (HARD ) HARVARD COLLEGE.

XX Celeste AJ, Melton DA, Rosen VA, Thomson GH, Wollman NM;

XX Wozney JM;

XX WPI: 1995-224420/29.

XX N-PSDB; AAQ96209.

XX Bone morphogenetic proteins -12 and -13 and corresp. DNA used in

XX compsn. for inducing tendon/ligament-like tissue formation

XX Example: Page 51-52; 84pp; English.

XX Oligos #6 and #7 (AAQ96218 & AAQ96219) are used as primers for the  
 CC amplification of a 275 bp DNA probe, the internal 269 bp of which  
 CC corresp. to nt5 #607 to #865 of AAQ96207, from the BMP-12 encoding  
 CC plasmid subclone PCR1-1#2. This probe was radioactively labelled  
 CC and used to screen a murine genomic library. DNA sequence analysis  
 CC of one of positively hybridising recombinants named MVR23 indicates  
 CC that it encodes a portion of the mouse gene corresp. to the PCR  
 CC product mV9 (murine homolog of the MP-52 sequence AAQ96209/R78741).

XX Sequence 120 AA;

Query Match 99.4%; Score 645; DB 16; Length 120;

Best Local Similarity 99.2%; Pred. No. 10-59; Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATKCKKPSKKNLKARSKKALHVNFKMGWDGWIAPLEYAFBCEGLCEPPLKSHLE 60  
 III

DB 2 platrqrkpsknlkarskalkhntkdmqwdwllapleyatheaqlcetpirshle 61  
 III

QY 61 PINHAVIQLMNSMDPESTPTACVPTRLSPISILFIDSANNVVKQYEDMVVSESGTR 119  
 III

DB 62 ptnhaviqlmnsmdpestptceptrlspisilfidsannvvykqyedmvseseqr 120  
 III

RESULT 5

AAW26590

ID AAW26590 standard; Protein: 120 AA.

XX AAW26590:

XX 21-JAN-1998 (first entry)

XX Human MP52 protein.

XX MP52; BMP; bone morphogenetic protein; human; tendon; ligament;  
 KW wound healing; tissue repair; tendonitis; carpal tunnel syndrome;  
 KW therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Protein 1..120

XX Protein /note= "Claim 5"

XX Protein /note= "Claim 5"

XX US5658882-A.

XX 19-AUG-1997.

XX 07-DEC-1994; 94US-0164104.

XX 22-DEC-1994; 94US-0362670.

XX 07-DEC-1994; 94US-0164103.

XX 25-MAR-1994; 94US-0217780.

XX 02-NOV-1994; 94US-0333576.

XX (GEMMY ) GENETICS INST INC.

XX (HARD ) HARVARD COLLEGE.

XX Celeste AJ, Melton DA, Rosen VA, Thomson GH, Wollman NM;

XX Wozney JM;

XX WPI: 1997-424270/49.

XX Inducing tendon and ligament formation using BMP 12, BMP 13 or MP 52

XX - useful for tissue healing and repair, treatment of tendonitis,

XX improving fixation of tendons to bone etc

XX Claim 5; Column 39-40; 4pp; English.

XX This polypeptide comprises human MP52. A claimed method for  
 CC inducing formation of tendon and/or ligament tissues involves the  
 CC administration of a composition containing at least one protein  
 CC selected from MP52, BMP-12 (see AAW26589) and BMP-13 (see AAW26591).

XX The method is used for tissue (including skin) healing and repair.

XX This is useful for treating tendonitis, carpal tunnel syndrome and

XX other defects of traumatic or congenital origin, in cosmetic

XX surgery and to improve fixation of tendons or ligaments to bone.

XX The specified proteins can also be used to increase activity of other  
 CC BMPs e.g. BMP-2 (see AAW26597).

XX Sequence 120 AA;



AAW46100  
ID AAW46100 standard; Protein: 501 AA.

AC AAW46100;

DT 08-MAY-1998 (first entry)

DE Human MP52.

KW Bone morphogenetic protein; BMP; processing enzyme; MP52;  
KW BMP-2; BMP-4; BMP-6; BMP-7; bone formation; bone regeneration.

OS Homo sapiens.

PN W09741250-A1.

PD 06-NOV-1997.

XX 28-APR-1997; 97W01JP01474.

XX 30-APR-1996; 96JP-0140618.

FA (FAH) HOECHST YAKUHIN KOGYO KK.

FA (FAH) HOECHST PHARM & CHEM KK.

XX Kimura M, Makishima F, Takahashi M;

XX WPI: 1997-54748/50.

DR N-PSDB; AAT98191.

XX production of mature bone morphogenetic protein - by treatment of  
PT precursor protein with a processing enzyme such as furin either  
PT directly or by expressing them both in the same host

XX Example 1; Pages 21-25; 4pp; Japanese.

XX The present sequence is MP52, which is a bone morphogenetic  
CC protein (BMP).

CC Mature BMP can be produced by directly adding a BMP processing  
CC enzyme to a solution containing BMP precursor protein, or by  
CC transforming an animal cell with expression vectors containing DNA  
CC encoding the enzyme and precursor protein, culturing the  
CC transformant and isolating the mature BMP from the culture. The  
CC method can be used to produce MP52, BMP-2, BMP-4, BMP-6 and BMP-7,  
CC which can be used to treat bone formation or regeneration  
CC abnormalities.

XX Sequence 501 AA:

Query Match 99.4%; Score 645; DB 18; Length 501;  
Best Local Similarity 99.2%; Pred. No. 5,90-59;  
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATRGCKRPSKNIKARCSKALHVNFKDMQWIDWIIAPLEYEAFHCHGJCEPPLRSHLE 60  
ID 384 platrqkripsknlkarcskalkhvnfkdmqwdwiiapleyeafhchgeclplrshle 442

QY 61 PTNHAVIQTLMNSMDPESTPTTACVPTRLSPISILFIDSANNVYKQYEMVVSQGR 119  
ID 443 plnhaviqtlnmsmdpestpttccvptrlspisilfidsannvvykqyedmvvsqgr 501

RESULT 9

AAW19210

ID AAW19210 standard; Protein: 501 AA.

AC AAW19210;

DT 04-MAR-1998 (first entry)

XX Human TGF-beta protein MP52.

XX

KW Human transforming growth factor-beta; TGF-beta; MP52; superfamily;  
KW cartilage; bone inducing activity; inhibit; bone resorption.

OS Homo sapiens.

PN DE19548476-A1.

PD 26-JUN-1997.

XX 22-DEC-1995; 95DE-1048476.

PR 22-DEC-1995; 95DE-1048476.

PA (H10P-) BIOBAHM GES BIOTECHNOLOGISCHEN ENTWICKL.

XX Bechtold R, Botton G, Paulista M, Pohl J, Roetten G;

XX WPI: 1997-338941/41.

DR N-PSDB; AA169095.

XX Compound containing protein from TGF-beta superfamily has bone  
PT and/or cartilage inducing activity, useful in treatment of, e.g.  
PT osteoporosis, bone damage, Paget's disease and osteoarthritis

XX Claim 3; Page 9; 10pp; German.

XX This sequence is the human transforming growth factor (TGF)-beta protein  
CC designated MP52. MP52 can be used in a compound of formula (I):  
CC A-X(1-20) B(1-20) (I); A = protein, or fragment, of the TGF-beta  
CC superfamily with cartilage and/or bone inducing activity (e.g. MP52);  
CC B = 1 or more substituent groups with an affinity to the extracellular  
CC matrix, cellular components of bone and/or cartilage and/or to a  
CC biocompatible carrier matrix; X = 1 or more covalent bonds and/or spacer  
CC groups. The compound may be used to inhibit bone resorption, prevent or  
CC treat bone or cartilage related disorders, including osteoporosis,  
CC Paget's disease, osteodystrophy, osteoarthritis or osteoarthritis and  
CC to treat bone or cartilage damage caused by wounding or overloading.

XX Sequence 501 AA:

Query Match 99.4%; Score 645; DB 18; Length 501;  
Best Local Similarity 99.2%; Pred. No. 5,90-59;  
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATRGCKRPSKNIKARCSKALHVNFKDMQWIDWIIAPLEYEAFHCHGJCEPPLRSHLE 60  
ID 384 platrqkripsknlkarcskalkhvnfkdmqwdwiiapleyeafhchgeclplrshle 442

QY 61 PTNHAVIQTLMNSMDPESTPTTACVPTRLSPISILFIDSANNVYKQYEMVVSQGR 119  
ID 443 plnhaviqtlnmsmdpestpttccvptrlspisilfidsannvvykqyedmvvsqgr 501

RESULT 10

AAW11900

ID AAW11900 standard; Protein: 501 AA.

XX AAW11900;

DT 28-OCT-1997 (first entry)

XX Human high mol. wt. protein MP52, a growth/differentiation factor.

XX Growth factor; differentiation; bone induction; osteoporosis; teeth;  
KW tooth; dental; joint tissue; cartilage; mucous membrane; skin; nails;  
KW wound healing; regeneration; skeletal disorder; fracture; dimer.

OS Homo sapiens.

XX W09704095 A1.

XX 06-FEB-1997.



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CC replacement. The implant has cartilage and/or bone-forming activity and
CC can be used for local treatment of cartilage and/or bone diseases or
CC damage caused by trauma, surgery, degeneration or overloading. The
CC implant can also be used for the treatment of bone defects, e.g.,
CC parodontitis or fractures and in cosmetic and plastic surgery for fixing
CC mobile bones.
XX
SQ Sequence 501 AA;

Query Match 99.4%; Score 645; DB 19; Length 501;
Best Local Similarity 99.2%; Prod.No. 5,9e 59;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLAIKGRKRSKNLKARCSKKALHVNFKDGMJDMIIAPLEYEAFHGEGICEFPIRSHLE 60
DB 383 plaiqrkrskskalrcskalkhvnfkdgmdwdmiiapleyeahceqicefpirshle 442
QY 61 PINHAVIQTINSMDSPEPTPAVPTPLSPISILFDISANNVVYKYVEDMMVSESQGR 119
DB 443 pinhavigtinmsmdpsptpeptplspisilfdisanvvykyedmmvsesqgr 501

RESULT 14
AAW34008
ID AAW34008 standard; Protein: 501 AA.
AC AAW34008;
XX
XX
DI 22-MAY-1998 (first entry)
XX
XX Human MP52.
XX
XX Human MP52; mouse monoclonal antibody; MAb; purification;
KW assayng.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..27
FT /label seq_peptide
FT Peptide 28..501
FF /label mat_peptide
XX
XX W0974-408 AI.
XX
XX Z0-Nov-1997.
XX
XX 14-MAY-1997; 97W0-JP01603.
XX
XX 07-MAY-1997; 97JP-0141641.
PR 14-MAY-1996; 96JP-0141147.
XX
XX (PARH ) HEPHST PHARM & CHEM KK.
FA
XX
XX Jitsukawa I, Kitadawa H, Nakatowa H, Yamahisawa S.
XX
XX WP1: 1998-008877/01.
DR N-PSUH; AA188340.
XX
XX Mouse anti-human MP52 monoclonal antibody - recombinates the dimeric
FT form of MP52 but not the monomer, and does not cross-react with
PT TGF-beta or BMP-2
XX
XX Disclosure; Pages 41-45; 46pp; Japanese.
FS
XX
XX The present sequence, human MP52, was used in the
CC preparation of a novel mouse monoclonal antibody (MAb), which
CC recombinates dimeric but not monomeric human MP52. The MAb has a
CC heavy chain of subclass gamma2, and does not cross react with
CC IgG-beta or BMP-2. The MAb may be used to purify and assay human
CC MP52, especially recombinant MP52.
XX
XX

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OM protein - protein search, using sw model

Run on: March 26, 2002, 06:09:02 : Search time 12.55 Seconds  
(without alignments)  
213.478 Million cell updates/sec

Title: US-09-701-121-2  
Perfect score: 645  
Sequence: 1 PLATROCKRPSKMLKARCSK.....ANNVYKQVEMVMSVSGR 119  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22504292 residues  
Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents-AA\*  
1: /cqn2\_6/ptodata/2/1aa/5A\_00MB.pep.\*  
2: /cqn2\_6/ptodata/2/1aa/5B\_00MB.pep.\*  
3: /cqn2\_6/ptodata/2/1aa/6A\_00MB.pep.\*  
4: /cqn2\_6/ptodata/2/1aa/6B\_00MB.pep.\*  
5: /cqn2\_6/ptodata/2/1aa/PTCUS\_COMB.pep.\*  
6: /cqn2\_6/ptodata/2/1aa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
1	645	99.4	120	1 US-08-362-670B-4	Sequence 4, Appl
2	645	99.4	120	3 US-08-333-576C-4	Sequence 4, Appl
3	645	99.4	120	4 US-08-808-324-4	Sequence 4, Appl
4	645	99.4	120	5 PCT-US94-14030A-4	Sequence 4, Appl
5	645	99.4	401	3 US-08-289-222E-3	Sequence 3, Appl
6	645	99.4	401	4 US-09-054-536B-3	Sequence 3, Appl
7	645	99.4	501	2 US-08-288-508C-2	Sequence 2, Appl
8	640	98.6	119	1 US-08-455-559-13	Sequence 13, Appl
9	640	98.6	119	4 US-09-145-060-13	Sequence 13, Appl
10	640	98.6	119	5 PCT-US94-00657-13	Sequence 13, Appl
11	640	98.6	495	1 US-08-455-559-10	Sequence 10, Appl
12	640	98.6	495	4 US-09-145-060-10	Sequence 10, Appl
13	640	98.6	495	5 PCT-US94-00657-10	Sequence 10, Appl
14	559	86.1	102	1 US-08-345-584C-51	Sequence 51, Appl
15	559	86.1	102	2 US-08-288-508C-13	Sequence 13, Appl
16	559	86.1	102	3 US-08-289-222E-22	Sequence 22, Appl
17	559	86.1	102	4 US-09-054-536B-22	Sequence 22, Appl
18	543	83.7	119	1 US-08-581-529B-7	Sequence 7, Appl
19	543	83.7	119	3 US-09-097-616-7	Sequence 7, Appl
20	543	83.7	119	5 PCT-US94-07762-7	Sequence 7, Appl
21	543	83.7	134	1 US-08-581-524B-6	Sequence 6, Appl
22	543	83.7	134	3 US-09-097-616-6	Sequence 6, Appl
23	543	83.7	134	5 PCT-US94-07762-6	Sequence 6, Appl
24	540	83.2	321	1 US-08-362-670B-26	Sequence 26, Appl
25	540	83.2	321	3 US-08-333-576C-26	Sequence 26, Appl
26	540	83.2	321	4 US-08-808-324-26	Sequence 26, Appl
27	540	83.2	321	5 PCT-US94-14030A-26	Sequence 26, Appl

28	548	82.9	263	1 US-08-362-670B-42	Sequence 42, Appl
29	548	82.9	263	3 US-08-333-576C-42	Sequence 42, Appl
30	548	82.9	263	4 US-08-808-324-42	Sequence 42, Appl
31	548	82.9	263	5 PCT-US94-14030A-42	Sequence 42, Appl
32	494	76.1	129	1 US-08-360-914B-15	Sequence 15, Appl
33	494	76.1	129	1 US-08-741-589A-13	Sequence 13, Appl
34	494	76.1	294	1 US-08-362-670B-2	Sequence 2, Appl
35	494	76.1	294	3 US-08-333-576C-2	Sequence 2, Appl
36	494	76.1	294	4 US-08-808-324-2	Sequence 2, Appl
37	494	76.1	294	5 PCT-US94-14030A-2	Sequence 2, Appl
38	494	76.1	388	1 US-08-362-670B-34	Sequence 34, Appl
39	494	76.1	388	3 US-08-333-576C-34	Sequence 34, Appl
40	494	76.1	388	4 US-08-808-324-34	Sequence 34, Appl
41	494	76.1	388	5 PCT-US94-14030A-34	Sequence 34, Appl
42	494	76.1	411	1 US-08-362-670B-28	Sequence 28, Appl
43	494	76.1	411	3 US-08-333-576C-28	Sequence 28, Appl
44	494	76.1	411	4 US-08-808-324-28	Sequence 28, Appl
45	494	76.1	411	5 PCT-US94-14030A-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1  
US-08-362-670B-4  
: Sequence 4, Application US/08362670B  
: Patent No. 5658882  
: GENERAL INFORMATION:  
: APPLICANT: Celesteo, Anthony J.  
: APPLICANT: Wozney, John  
: APPLICANT: Rosen, Vicki A.  
: APPLICANT: Wolman, Neil  
: APPLICANT: Ihmsen, Gerald H.  
: APPLICANT: Melton, Douglas A.  
: TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS  
: NUMBER OF SEQUENCES: 37  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: GENETIP'S INSTITUTE, INC.  
: STREET: 87 CambridgePark Drive  
: CITY: Cambridge  
: STATE: Massachusetts  
: COUNTRY: USA  
: ZIP: 02140  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: Patent In Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08362,670B  
: FILING DATE: December 22, 1994  
: CLASSIFICATION: 514  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Lazar, Steven R.  
: REGISTRATION NUMBER: 32,618  
: REFERENCE/INVENT NUMBER: 5202-D  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: 617 498-8260  
: TELEFAX: 617 876-5851  
: INFORMATION FOR SEQ ID NO: 4:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 120 amino acids  
: TYPE: amino acid  
: TOPOLOGY: linear  
: MOLECULE TYPE: protein  
: US-08-362-670B-4

Query Match 99.4% Score 645 DB 1 Length 120

Best Local Similarity 99.2% Pred. No. 9,36-65

Matches 119 Conservative 0 Mismatches 1 Labels 0 Gaps

1 PLATROCKRPSKMLKARCSKALHVNFKMGWIDWITAPLEYAFH-EGLTEFPLRSHE 60

DB 2 PLATPGKRSKNLKARSRKALHVNFKDMGMDWMTAPLEYEAFRCGLTEFFLSHLE 61  
 QY 61 PINHAVIQTLMNSMDESTPTTACVPTKSPISLFTLSANNVVKQYEDMVVVSQGR 119  
 DB 62 PINHAVIQTLMNSMDESTPTTCCVPTKSPISLFTLSANNVVKQYEDMVVVSQGR 120

## RESULT 2

US-09-701-121-2  
 ? Sequence 4, Application US/08435760  
 ? Patent No. 6027919  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Celvesto, Anthony J.  
 ? APPLICANT: Wozniak, John  
 ? APPLICANT: Roscoe, Vicki A.  
 ? APPLICANT: Wellman, Gerald H.  
 ? APPLICANT: McIlton, Douglas A.  
 ? TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS  
 ? NUMBER OF SEQUENCES: 47  
 ? CORRESPONDENCE ADDRESS:  
 ? ADDRESS: GENETICS INSTITUTE, INC.  
 ? STREET: 87 Cambridgepark Drive  
 ? CITY: Cambridge  
 ? STATE: Massachusetts  
 ? COUNTRY: USA  
 ? ZIP: 02140  
 ? COMPUTER READABLE FORM:  
 ? MEDIUM TYPE: Floppy disk  
 ? COMPUTER: IBM PC compatible  
 ? OPERATING SYSTEM: PC-DOS/MS-DOS  
 ? SOFTWARE: Patent in Release #1.0, Version #1.25  
 ? CURRENT APPLICATION DATA:  
 ? APPLICATION NUMBER: US/08/334,576  
 ? FILING DATE: No. 6027919, 2, 1994  
 ? CLASSIFICATION: 435  
 ? ATTORNEY/AGENT INFORMATION:  
 ? NAME: Lazar, Steven R.  
 ? REGISTRATION NUMBER: 42,618  
 ? REFERENCE/DOCKET NUMBER: 5202-B  
 ? TELECOMMUNICATION INFORMATION:  
 ? TELEPHONE: 617 498-8260  
 ? TELEFAX: 617 876-5851  
 ? INFORMATION FOR SEQ ID NO: 4:  
 ? SEQUENCE CHARACTERISTICS:  
 ? LENGTH: 120 amino acids  
 ? TYPE: amino acid  
 ? TOPOLOGY: Linear  
 ? MOLECULE TYPE: protein  
 ? US-09-701-121-2

Query Match: 99.4%; Score 645; DB 4; Length 120;  
 Best Local Similarity: 99.2%; Pred. No. 9, 40-65;  
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATPGKRSKNLKARSRKALHVNFKDMGMDWMTAPLEYEAFRCGLTEFFLSHLE 60  
 DB 2 PLATPGKRSKNLKARSRKALHVNFKDMGMDWMTAPLEYEAFRCGLTEFFLSHLE 61  
 QY 61 PINHAVIQTLMNSMDESTPTTACVPTKSPISLFTLSANNVVKQYEDMVVVSQGR 119  
 DB 62 PINHAVIQTLMNSMDESTPTTCCVPTKSPISLFTLSANNVVKQYEDMVVVSQGR 120

## RESULT 3

US-08-424-4  
 ? Sequence 4, Application US/08080424  
 ? Patent No. 6204872  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Celvesto, Anthony J.  
 ? APPLICANT: Wozniak, John

? APPLICANT: Roscoe, Vicki A.  
 ? APPLICANT: Wellman, Gerald H.  
 ? APPLICANT: McIlton, Douglas A.  
 ? TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS  
 ? NUMBER OF SEQUENCES: 45  
 ? CORRESPONDENCE ADDRESS:  
 ? ADDRESS: GENETICS INSTITUTE, INC.  
 ? STREET: 87 Cambridgepark Drive  
 ? CITY: Cambridge  
 ? STATE: Massachusetts  
 ? COUNTRY: USA  
 ? ZIP: 02140  
 ? COMPUTER READABLE FORM:  
 ? MEDIUM TYPE: Floppy disk  
 ? COMPUTER: IBM PC compatible  
 ? OPERATING SYSTEM: PC-DOS/MS-DOS  
 ? SOFTWARE: Patent in Release #1.0, Version #1.25  
 ? CURRENT APPLICATION DATA:  
 ? APPLICATION NUMBER: US/08/808,424  
 ? FILING DATE: Berowith  
 ? CLASSIFICATION: 514  
 ? ATTORNEY/AGENT INFORMATION:  
 ? NAME: Lazar, Steven R.  
 ? REGISTRATION NUMBER: 42,618  
 ? REFERENCE/DOCKET NUMBER: 5202-B  
 ? TELECOMMUNICATION INFORMATION:  
 ? TELEPHONE: 617 498-8260  
 ? TELEFAX: 617 876-5851  
 ? INFORMATION FOR SEQ ID NO: 4:  
 ? SEQUENCE CHARACTERISTICS:  
 ? LENGTH: 120 amino acids  
 ? TYPE: amino acid  
 ? TOPOLOGY: Linear  
 ? MOLECULE TYPE: protein  
 ? US-08-808-424

Query Match: 99.4%; Score 645; DB 4; Length 120;  
 Best Local Similarity: 99.2%; Pred. No. 9, 40-65;  
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATPGKRSKNLKARSRKALHVNFKDMGMDWMTAPLEYEAFRCGLTEFFLSHLE 60  
 DB 2 PLATPGKRSKNLKARSRKALHVNFKDMGMDWMTAPLEYEAFRCGLTEFFLSHLE 61  
 QY 61 PINHAVIQTLMNSMDESTPTTACVPTKSPISLFTLSANNVVKQYEDMVVVSQGR 119  
 DB 62 PINHAVIQTLMNSMDESTPTTCCVPTKSPISLFTLSANNVVKQYEDMVVVSQGR 120

## RESULT 4

US-94-14040-4  
 ? Sequence 4, Application US/9414040A  
 ? GENERAL INFORMATION:  
 ? APPLICANT: GENETICS INSTITUTE, INC.  
 ? APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE  
 ? TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS  
 ? NUMBER OF SEQUENCES: 45  
 ? CORRESPONDENCE ADDRESS:  
 ? ADDRESS: GENETICS INSTITUTE, INC.  
 ? STREET: 87 Cambridgepark Drive  
 ? CITY: Cambridge  
 ? STATE: Massachusetts  
 ? COUNTRY: USA  
 ? ZIP: 02140  
 ? COMPUTER READABLE FORM:  
 ? MEDIUM TYPE: Floppy disk  
 ? COMPUTER: IBM PC compatible  
 ? OPERATING SYSTEM: PC-DOS/MS-DOS  
 ? SOFTWARE: Patent in Release #1.0, Version #1.25  
 ? CURRENT APPLICATION DATA:  
 ? APPLICATION NUMBER: US/94/14040A

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? FILING DATE: Herewith
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/164,104
? FILING DATE: 07-DEC-1993
? APPLICATION NUMBER: US 08/217,780
? FILING DATE: 25-MAR-1994
? APPLICATION NUMBER: US 08/443,576
? FILING DATE: 02-NOV-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: Lazar, Steven R.
? REGISTRATION NUMBER: 42,618
? REFERENCE/DOCKET NUMBER: 52020-PCT
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 617 498-5260
? TELEFAX: 617 876-5851
? INFORMATION FOR SEQ ID NO: 4:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 120 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? PCT-US94-14030A-4

Query Match 99.4%; Score 645; DB 5; length 120;
Best local Similarity 99.2%; Pred. No. 9, 4e-65;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROCKRKPSKNIKARCSRKALHVNFKDGMGWDWIITAPLEYAFHCEGLFPLRSHLE 60
DB 2 PLATROCKRKPSKNIKARCSRKALHVNFKDGMGWDWIITAPLEYAFHCEGLFPLRSHLE 61
QY 61 PTNHAIVQILMNSMDPESTPTACVPTRLSPISILFIDSANNVVKYEDMVVESGCR 119
DB 62 PTNHAIVQILMNSMDPESTPTACVPTRLSPISILFIDSANNVVKYEDMVVESGCR 120

RESULT 5
US-08-289-222E-4
? Sequence 3, Application US/08289222E
? Patent No. 6120760
? GENERAL INFORMATION:
? APPLICANT: HOTTEN, GERTRUD
? APPLICANT: NEIDHARDT, HELGE
? APPLICANT: RECHTOLD, ROLF
? APPLICANT: POHL, JENS
? TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF B
? NUMBER OF SEQUENCES: 53
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: NIKALDO, MARMELESTEIN, MURRAY & ORAM
? STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
? STREET: SUITE 400
? CITY: WASHINGTON
? STATE: DC
? COUNTRY: USA
? ZIP: 20005-5701
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent in Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/289,222E
? FILING DATE: 25-AUG-1999
? CLASSIFICATION: 424
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/289,222
? FILING DATE: 12-AUG-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: DE P 44 23 190.4
? FILING DATE: 07-JUL-1994

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? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: EP9 92102424.8
? FILING DATE: 12-FEB-1992
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: PCT/EP93/00350
? FILING DATE: 12-FEB-1993
? ATTORNEY/AGENT INFORMATION:
? NAME: KITTIS, MONICA CHIN
? REGISTRATION NUMBER: 36,105
? REFERENCE/DOCKET NUMBER: P564-0021
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 202/638-5000
? TELEFAX: 202/638-4810
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 401 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-289-222E-3

Query Match 99.4%; Score 645; DB 4; length 401;
Best local Similarity 99.2%; Pred. No. 4, 2e-64;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROCKRKPSKNIKARCSRKALHVNFKDGMGWDWIITAPLEYAFHCEGLFPLRSHLE 60
DB 283 PLATROCKRKPSKNIKARCSRKALHVNFKDGMGWDWIITAPLEYAFHCEGLFPLRSHLE 61
QY 61 PTNHAIVQILMNSMDPESTPTACVPTRLSPISILFIDSANNVVKYEDMVVESGCR 119
DB 343 PTNHAIVQILMNSMDPESTPTACVPTRLSPISILFIDSANNVVKYEDMVVESGCR 401

RESULT 6
US-09-054-524B-4
? Sequence 3, Application US/09054526B
? Patent No. 6197560
? GENERAL INFORMATION:
? APPLICANT: HITTEN, GERTRUD
? APPLICANT: NEIDHARDT, HELGE
? APPLICANT: RECHTOLD, ROLF
? APPLICANT: POHL, JENS
? TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
? TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS
? NUMBER OF SEQUENCES: 53
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: NIKALDO, MARMELESTEIN, MURRAY & ORAM LLP
? STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
? STREET: SUITE 330
? CITY: WASHINGTON
? STATE: DC
? COUNTRY: USA
? ZIP: 20005-5701
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent in Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/054,526B
? FILING DATE: 03-AUG-1998
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/289,222
? FILING DATE: 12-AUG-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: DE P 44 23 190.4
? FILING DATE: 01-JUL-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: EP9 92102424.8
? FILING DATE: 12-FEB-1992

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```

? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: PCT/EP94/00450
? FILING DATE: 12-FEB-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: KLITS, MONICA CHIN
? REGISTRATION NUMBER: 46,105
? REFERENCE/DOCKET NUMBER: P564 8005
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 202/638 5000
? TELEFAX: 202/638 4810
? INFORMATION FOR SEQ ID NO: 4:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 401 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-09-054 526B-4

Query Match          99.4%; Score 645; ID 4; Length 401;
Best Local Similarity 99.2%; Prod. No. 4-20-64;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATQGRKRSKNIKARSRKALHVNFKIMWDMWLLAPLEYEAFHCEGLCEPPLRSKLE 60
Db 283 PLATQGRKRSKNIKARSRKALHVNFKIMWDMWLLAPLEYEAFHCEGLCEPPLRSKLE 342

QY 61 PTNHAVIQTILNMSDPESTPTTACVPTPLSPSTLFDLSANNVYKQYEMVVESSGR 119
Db 443 PTNHAVIQTILNMSDPESTPTTACVPTPLSPSTLFDLSANNVYKQYEMVVESSGR 401

RESULT 7
US-09-288 508C-2
? Sequence 2; Application US/08288508C
? Patent No. 5994694
? GENERAL INFORMATION:
? APPLICANT: HUGO, Gottfried
? APPLICANT: Neidhardt, Helge
? APPLICANT: Paulista, Michael
? TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATING FACTOR OF
? TITLE OF INVENTION: THE TGF- FAMILY
? NUMBER OF SEQUENCES: 40
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Nikaido, Marmelstein, Murray & Gram LLP
? STREET: 655 Fifteenth Street N.W., Suite 440
? CITY: Washington
? STATE: D.C.
? COUNTRY: U.S.A.
? ZIP: 20005 5701
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC DOS/MS DOS
? SOFTWARE: Patent Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/288,508C
? FILING DATE: 10-AUG-1994
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: DE P 44 26 829.4
? FILING DATE: 10-AUG-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: DE P 44 18 222.8
? FILING DATE: 25-MAY-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: DE P 44 20 157.5
? FILING DATE: 09-JUN-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: JAHNS, Kristina M.
? REGISTRATION NUMBER: P-41,092
? REFERENCE/DOCKET NUMBER: P564 4019

```

```

? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (202)638 5000
? TELEFAX: (202)638 4810
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 501 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-288 508C-2

Query Match          99.4%; Score 645; ID 2; Length 501;
Best Local Similarity 99.2%; Prod. No. 5-60-64;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATQGRKRSKNIKARSRKALHVNFKIMWDMWLLAPLEYEAFHCEGLCEPPLRSKLE 60
Db 483 PLATQGRKRSKNIKARSRKALHVNFKIMWDMWLLAPLEYEAFHCEGLCEPPLRSKLE 442

QY 61 PTNHAVIQTILNMSDPESTPTTACVPTPLSPSTLFDLSANNVYKQYEMVVESSGR 119
Db 443 PTNHAVIQTILNMSDPESTPTTACVPTPLSPSTLFDLSANNVYKQYEMVVESSGR 401

RESULT 8
US-08-455 559-13
? Sequence 13; Application US/08455559
? Patent No. 5401014
? GENERAL INFORMATION:
? APPLICANT: LEE, SE JIN
? APPLICANT: HUYNH, THANH
? TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR 5
? NUMBER OF SEQUENCES: 27
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: SPENSLEY BORN JIHAS & LORTIZ
? STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
? CITY: LOS ANGELES
? STATE: CALIFORNIA
? COUNTRY: US
? ZIP: 90067
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC DOS/MS Dos
? SOFTWARE: Patent Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/455,559
? FILING DATE: 31-MAY-1995
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US-08/003,144
? FILING DATE: 12-JAN-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: WETTERELL, JR., PH.D., JOHN R.
? REGISTRATION NUMBER: 41,678
? REFERENCE/DOCKET NUMBER: P42280
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 619/455-5100
? TELEFAX: 619 455 5110
? INFORMATION FOR SEQ ID NO: 13:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 119 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? IMMEDIATE SOURCE:
? CLONE: GDF 5
? FEATURE:
? NAME/KEY: protein
? LOCATION: 1..119
? US-08-455 559-13

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Query Match      98.6%; Score 640; DB 1; Length 119;
Best Local Similarity 98.4%; Pred. No. 3,40-64;
Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLATGKGRPSKNLKARCSRKALHVNFKDMGWDMWIIAPLEYEAFHCEGLCEFFLRSHLE 60
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DB 1 PLANRQGRPSKNLKARCSRKALHVNFKDMGWDMWIIAPLEYEAFHCEGLCEFFLRSHLE 60
   IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII

QY 61 PINHAVIQTLMNSMDPESTPTTACVPTRLSPSTILFIDSANNVVKQYEDMWWVESGCR 119
   IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
DB 61 PINHAVIQTLMNSMDPESTPTTACVPTRLSPSTILFIDSANNVVKQYEDMWWVESGCR 119
   IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII

RESULT 9
US-09-145-060-14
: Sequence 14, Application US/09145060
: Patent No. 6245895
: GENERAL INFORMATION:
: APPLICANT: LEE, SE-JIN
: APPLICANT: HUYNH, THANH
: TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
: NUMBER OF SEQUENCES: 27
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson, P.C.
: STREET: 4225 Executive Square, Suite 1400
: CITY: La Jolla
: STATE: CA
: COUNTRY: USA
: ZIP: 92037
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: Windows95
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/145,060
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/455,559
: FILING DATE: 31-MAY-1995
: APPLICATION NUMBER: 08/003,144
: FILING DATE: 12-JAN-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Lisa A. Haille, Ph.D.
: REGISTRATION NUMBER: 38,347
: REFERENCE/DOCKET NUMBER: 07265/057001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619/678-5070
: TELEFAX: 619/678-5099
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 119 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: IMMEDIATE SOURCE:
: CLONE: GDF-5
US-09-145-060-14

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Query Match      98.6%; Score 640; DB 5; Length 119;
Best Local Similarity 98.4%; Pred. No. 3,40-64;
Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLATGKGRPSKNLKARCSRKALHVNFKDMGWDMWIIAPLEYEAFHCEGLCEFFLRSHLE 60
   IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
DB 1 PLANRQGRPSKNLKARCSRKALHVNFKDMGWDMWIIAPLEYEAFHCEGLCEFFLRSHLE 60
   IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII

QY 61 PINHAVIQTLMNSMDPESTPTTACVPTRLSPSTILFIDSANNVVKQYEDMWWVESGCR 119
   IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
DB 61 PINHAVIQTLMNSMDPESTPTTACVPTRLSPSTILFIDSANNVVKQYEDMWWVESGCR 119
   IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII

RESULT 11
US-08-455-559-10
: Sequence 10, Application US/08455559
: Patent No. 5801014
: GENERAL INFORMATION:
: APPLICANT: LEE, SE-JIN
: APPLICANT: HUYNH, THANH
: TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
: NUMBER OF SEQUENCES: 27
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SPENSLEY BORN JUBAS & LOHITZ
: STREET: 1860 CENTURY PARK EAST, FIFTH FLOOR
: CITY: LOS ANGELES
: STATE: CALIFORNIA
: COUNTRY: US
: ZIP: 90067
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/00657
: FILING DATE: 1/12/94
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: WETTERELL, JR. PH.D., JOHN K.
: REGISTRATION NUMBER: 41,678
: REFERENCE/DOCKET NUMBER: ED4256 CIP OF P02280
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619/455-5100
: TELEFAX: 619-455-5110
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 119 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: IMMEDIATE SOURCE:
: CLONE: GDF-5
: FEATURE:
: NAME/KEY: Protein
: LOCATION: 1..119
PCT-US94-00657-13

```









GenCore version 4.5  
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OW protein - protein search, using sw model

Run on: March 26, 2002, 06:09:02 ; Search time 14.35 seconds  
(without alignments)  
631,691 Million cell updates/sec

Title: US-09-701-121-2  
Perfect score: 649  
Sequence: 1 PLATROGKRFSSKNLKARCSR.....ANNVYKQYEMVVSQGR 119  
Scoring table: BLASTM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR68:  
1: pir1:  
2: pir2:  
3: pir3:  
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

				SUMMARIES	
Result No.	Score	Query Match	Length DB ID	Description	
1	645	99.4	501 2 JC2347	growth/differentia	
2	640	98.6	495 2 S43294	bone morphogenetic	
3	639	98.5	501 2 A55452	cartilage-derived	
4	543	83.7	125 2 S43295	bone morphogenetic	
5	528	81.4	436 2 B55452	cartilage-derived	
6	493	76.0	151 2 S43296	bone morphogenetic	
7	353.5	54.5	461 2 S52408	SPDVR1 protein - s	
8	347	53.5	393 2 S37073	bone morphogenetic	
9	347	53.5	394 2 S45355	bone morphogenetic	
10	347	53.5	395 1 BMH02	bone morphogenetic	
11	347	53.5	401 2 JH0689	bone morphogenetic	
12	346	53.4	400 2 A49147	bone morphogenetic	
13	346	53.3	405 2 I50608	bone morphogenetic	
14	344	53.0	588 2 A26158	decapentaplegic pr	
15	343	52.9	398 2 JH0688	bone morphogenetic	
16	343	52.9	398 2 JH0687	bone morphogenetic	
17	341	52.1	408 2 S48343	bone morphogenetic	
18	341	52.5	420 2 I49541	bone morphogenetic	
19	339	52.2	408 1 BMH04	bone morphogenetic	
20	338	52.1	408 2 S58791	bone morphogenetic	
21	337	51.9	353 2 I50607	bone morphogenetic	
22	334	51.3	207 2 S47618	var protein - rat	
23	333	51.3	452 2 I49542	bone morphogenetic	
24	333	51.3	454 1 BMH05	bone morphogenetic	
25	332	51.2	513 1 BMH06	bone morphogenetic	
26	331	51.0	408 2 JH0801	bone morphogenetic	
27	330	50.8	413 2 I51284	bone morphogenetic	
28	330	50.8	431 1 BMH07	bone morphogenetic	
29	329	50.7	510 2 A54798	V4-1-related prote	

bone morphogenetic  
osteogenic protein  
osteogenic protein  
Val embryonic grow  
cell-1 protein - Ca  
TGF-beta-related p  
TGF-beta homolog d  
growth/differentia  
bone morphogenetic  
bone morphogenetic  
transforming growt  
TGF-beta-related p  
GDF-1 embryonic ar  
bone morphogenetic  
GDF-1 embryonic ar  
bone morphogenetic

RESULT 1  
JC2347  
growth/differentiation factor 5 - human  
C:Species: Homo sapiens (man)  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 17-Mar-2000  
C:Accession: J02347  
R:Hoetten, G.; Neidhardt, H.; Jacobowsky, B.; Pahl, J.  
Biochem. Biophys. Res. Commun. 204, 646-652, 1994  
A:Title: Cloning and expression of recombinant human growth/differentiation factor 5.  
A:Reference number: J02347  
A:Accession: J02347; M010:95071475  
A:Molecule type: DNA  
A:Residues: 1-501 stop.  
A:Cross-references: GB:X80915; NID:4671524; PIDD:CAA56874.1; PIDD:4671525.  
C:Genetic:  
A:Gene: GDF-BMP9  
A:Cross-references: GDF:433948  
A:Introns: 211/1  
C:Superfamily: Inhibin  
C:Keywords: glycoprotein  
F:189/Binding site: carbonylhydrate (Asn) (covalent) #status predicted  
F:381-382/Cleavage site: Arg-Ala (unidentified proteinase) #status predicted

ALIGNMENTS

Query Match 99.4% Score 645; DB 2; Length 501;  
Best Local Similarity 99.2% Pred. No. 2.9e-5%  
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGKRFSSKNLKARCSRKALHVNFKDMGDDWITAPLEYAFHCEGLCEPILRSBLE 60  
|||||  
DB 383 PLATROGKRFSSKNLKARCSRKALHVNFKDMGDDWITAPLEYAFHCEGLCEPILRSBLE 442

QY 61 PTNHAIVQILMNSMDPESTPTTACVPTRLSPISILFIDSANNVYKQYEMVVSQGR 119  
|||||  
DB 443 PTNHAIVQILMNSMDPESTPTTACVPTRLSPISILFIDSANNVYKQYEMVVSQGR 501

RESULT 2  
S43294  
bone morphogenetic protein related protein (GDF5) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 20-Oct-1994 #sequence\_revision 10-Nov-1995 #text\_change 17-Mar-2000  
C:Accession: S43294  
R:Storm, E.E.; Hayib, I.V.; Copeland, N.G.; Jenkins, N.A.; Kinzler, D.M.; Lee, S.H.  
Nature 368, 639-643, 1994  
A:Title: Limb alterations in brachypodism mice due to mutations in a new member of th  
A:Reference number: S43294; M010:94195427  
A:Accession: S43294  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-495 stop.  
A:Cross-references: GB:X008337; NID:4486061; PIDD:AAA18778.1; PIDD:4486062

C:Superfamily: inhibin

Query Match 98.6%; Score 640; ID: 2; Length 495;  
 Best Local Similarity 98.3%; Pred. No. 9, 40, 59;  
 Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLATGCKRKRKSKNIKARCSKRALHVNFKDMGWDWIITAPLEYAFHFGEGEPTPLRSHELE 60  
 ID 1 PLATGCKRKRKSKNIKARCSKRALHVNFKDMGWDWIITAPLEYAFHFGEGEPTPLRSHELE 60  
 QY 477 PLNRGCKRKRKSKNIKARCSKRALHVNFKDMGWDWIITAPLEYAFHFGEGEPTPLRSHELE 446  
 ID 477 PLNRGCKRKRKSKNIKARCSKRALHVNFKDMGWDWIITAPLEYAFHFGEGEPTPLRSHELE 446

QY 61 PTHAVIQTLLNSMDPESTPTACVPTPLSPISITLFDSSANNVYKQYELMMVVSQGR 119  
 ID 61 PTHAVIQTLLNSMDPESTPTACVPTPLSPISITLFDSSANNVYKQYELMMVVSQGR 119  
 QY 447 PTHAVIQTLLNSMDPESTPTACVPTPLSPISITLFDSSANNVYKQYELMMVVSQGR 495  
 ID 447 PTHAVIQTLLNSMDPESTPTACVPTPLSPISITLFDSSANNVYKQYELMMVVSQGR 495

RESULT 3  
 A55452  
 cartilage-derived morphogenetic protein 1 precursor human  
 C:Species: Homo sapiens (man)  
 C:Date: 10-Feb-1995 #sequence\_revision 10-Feb-1995 #text\_change 17 Mar 2000  
 C:Accession: A55452

R.Chang, S.C.; Hoang, B.; Thomas, J.T.; Vukicevic, S.; Layton, F.P.; Kyba, N.J.P.; Kozak  
 J. Biol. Chem. 269, 28227-28244, 1994  
 A:Title: Cartilage-derived morphogenetic proteins. New members of the transforming growth  
 factor-beta family.

A:Reference number: A55452; M01D:95050604  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-501; CHA  
 A:Cross references: G01:0660; NID:q600741; PID:q600742  
 C:Genet res:  
 A:Gene: GDB:GIMPL  
 A:Cross reference: GDB:448940  
 C:Superfamily: inhibin

Query Match 98.5%; Score 639; ID: 2; Length 501;  
 Best Local Similarity 98.3%; Pred. No. 1, 20, 58;  
 Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLATGCKRKRKSKNIKARCSKRALHVNFKDMGWDWIITAPLEYAFHFGEGEPTPLRSHELE 60  
 ID 483 PSATGCKRKRKSKNIKARCSKRALHVNFKDMGWDWIITAPLEYAFHFGEGEPTPLRSHELE 442  
 QY 61 PTHAVIQTLLNSMDPESTPTACVPTPLSPISITLFDSSANNVYKQYELMMVVSQGR 119  
 ID 444 PTHAVIQTLLNSMDPESTPTACVPTPLSPISITLFDSSANNVYKQYELMMVVSQGR 501

RESULT 4  
 S43295  
 bone morphogenetic protein homolog glf6 precursor mouse (Tramont)  
 N:Alternative names: growth and differentiation factor 6  
 C:Species: Mus musculus (house mouse)  
 C:Date: 20-Oct-1994 #sequence\_revision 07-Feb-1997 #text\_change 26 May 2000  
 C:Accession: S43295

R.Strom, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kinzler, D.M.; Lee, S.J.  
 Nature 368, 639-643, 1994  
 A:Title: Limb alterations in brachypodism mice due to mutations in a new member of the  
 transforming growth factor-beta family.

A:Reference number: S43294; M01D:94195427  
 A:Accession: S43295  
 A:Molecule type: DNA  
 A:Residues: 1-125; SITO  
 A:Cross references: EMBL:008348; NID:q488465; PID:AAA18779.1; PID:q488464

C:Genet res:  
 A:Gene: GDB:6416  
 C:Superfamily: inhibin  
 F1:5/Domain: polybasic protease recognition site #status predicted +prp  
 F1:6/125/Product: bone morphogenetic protein homolog glf6 (Tramont) #status predicted +m

Query Match 84.7%; Score 544; ID: 2; Length 125;  
 Best Local Similarity 74.5%; Pred. No. 4, 60, 44;  
 Matches 83; Conservative 20; Mismatches 10; Indels 0; Gaps 0;

Best Local Similarity 80.3%; Pred. No. 2, 40, 49;  
 Matches 94; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 3 ATGCKRKRKSKNIKARCSKRALHVNFKDMGWDWIITAPLEYAFHFGEGEPTPLRSHELE 62  
 ID 3 ATGCKRKRKSKNIKARCSKRALHVNFKDMGWDWIITAPLEYAFHFGEGEPTPLRSHELE 62  
 QY 9 ASRRGCKRKRKSKNIKARCSKRALHVNFKDMGWDWIITAPLEYAFHFGEGEPTPLRSHELE 68  
 ID 9 ASRRGCKRKRKSKNIKARCSKRALHVNFKDMGWDWIITAPLEYAFHFGEGEPTPLRSHELE 68

QY 63 NHAVIQTLLNSMDPESTPTACVPTPLSPISITLFDSSANNVYKQYELMMVVSQGR 119  
 ID 63 NHAVIQTLLNSMDPESTPTACVPTPLSPISITLFDSSANNVYKQYELMMVVSQGR 119  
 QY 69 NHAVIQTLLNSMDPESTPTACVPTPLSPISITLFDSSANNVYKQYELMMVVSQGR 125  
 ID 69 NHAVIQTLLNSMDPESTPTACVPTPLSPISITLFDSSANNVYKQYELMMVVSQGR 125

RESULT 5  
 R55452  
 cartilage-derived morphogenetic protein 2 precursor bovine (Tramont)  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 10-Feb-1995 #sequence\_revision 10-Feb-1995 #text\_change 26 May 2000  
 C:Accession: R55452

J. Biol. Chem. 269, 28227-28244, 1994  
 A:Title: Cartilage-derived morphogenetic proteins. New members of the transforming growth  
 factor-beta family.

A:Reference number: A55452; M01D:95050604  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-446; CHA  
 A:Cross references: G01:0661; NID:q642489; PID:AAA1816.1; PID:q642490  
 C:Superfamily: inhibin

Query Match 81.4%; Score 528; ID: 2; Length 446;  
 Best Local Similarity 76.9%; Pred. No. 3, 50, 47;  
 Matches 90; Conservative 16; Mismatches 11; Indels 0; Gaps 0;

QY 3 ATGCKRKRKSKNIKARCSKRALHVNFKDMGWDWIITAPLEYAFHFGEGEPTPLRSHELE 62  
 ID 320 ASRRGCKRKRKSKNIKARCSKRALHVNFKDMGWDWIITAPLEYAFHFGEGEPTPLRSHELE 379  
 QY 63 NHAVIQTLLNSMDPESTPTACVPTPLSPISITLFDSSANNVYKQYELMMVVSQGR 119  
 ID 63 NHAVIQTLLNSMDPESTPTACVPTPLSPISITLFDSSANNVYKQYELMMVVSQGR 446

RESULT 6  
 S43296  
 bone morphogenetic protein related protein (glf7) mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 20-Oct-1994 #sequence\_revision 10-Nov-1995 #text\_change 19 May 2000  
 C:Accession: S43296

R.Strom, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kinzler, D.M.; Lee, S.J.  
 Nature 368, 639-643, 1994  
 A:Title: Limb alterations in brachypodism mice due to mutations in a new member of the  
 transforming growth factor-beta family.

A:Reference number: S43294; M01D:94195427  
 A:Accession: S43296  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-151; SITO  
 A:Cross references: G01:008349; NID:q488465; PID:AAA18780.1; PID:q488466  
 C:Superfamily: inhibin

Query Match 76.0%; Score 493; ID: 2; Length 151;  
 Best Local Similarity 74.5%; Pred. No. 4, 60, 44;  
 Matches 83; Conservative 20; Mismatches 10; Indels 0; Gaps 0;

QY 7 GRPKSKNIKARCSKRALHVNFKDMGWDWIITAPLEYAFHFGEGEPTPLRSHELE 66  
 ID 7 GRPKSKNIKARCSKRALHVNFKDMGWDWIITAPLEYAFHFGEGEPTPLRSHELE 66  
 QY 49 GRGCKRKRKSKNIKARCSKRALHVNFKDMGWDWIITAPLEYAFHFGEGEPTPLRSHELE 98  
 ID 49 GRGCKRKRKSKNIKARCSKRALHVNFKDMGWDWIITAPLEYAFHFGEGEPTPLRSHELE 98

QY 67 TGTLLNSMDPESTPTACVPTPLSPISITLFDSSANNVYKQYELMMVVSQGR 119  
 ID 67 TGTLLNSMDPESTPTACVPTPLSPISITLFDSSANNVYKQYELMMVVSQGR 151

## RESULT 7

S52408  
SPDWR1 protein - sea urchin (Strongylocentrotus purpuratus)

C:Species: Strongylocentrotus purpuratus (purple urchin)

C>Date: 08-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 20-Sep-1999

C:Accession: S52408

R:Source: M.R.: Micol, J.L.: Davidson, E.H.

submitted to the EMBL Data Library, February 1995

A:Description: SPDWR1, a member of the transforming growth factor-beta superfamily expressed

A:Reference number: S52408

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-461 #LEN>

A:Cross-references: EMBL:Z48313; NID:q673496; PID:q673497

C:Superfamily: inhibin

Query Match 53.5% Score 353.5; DB 2; Length 461;

Best Local Similarity 54.3%; Pred. No. 26-28;

Matches 63; Conservative 19; Mismatches 32; Indels 19; Gaps 2;

QY 3 ATRQ--CKRPSK-----NIKAKSRKALHVNFKDMGWDWIITAPLEYE 43

DB 426 ATRQKGGKRRKPPDINDIASRDSASSLSDWCKRKNIENVNFDLWQEWIITAPLGYY 485

QY 44 AFHCERGLFEPLRSHLEPTNHAIVQITLMSMDPESTPTACVPTRLSPSTILFIDSANNV 103

DB 486 AFYQGECAEPLNHNATNHAIVQITLHMSHSHVPPQCATKISPIITLVYIDSRNV 445

QY 104 VYKQVDMVVEGCG 118

DB 446 VLKKYKNVVRACG 460

## RESULT 8

S37073

bone morphogenetic protein 2 - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 16-Jul-1999

C:Accession: S37073

R:Refnd, J.O.: Chen, D.; Feng, M.; Harris, M.A.; Mundy, G.R.; Harris, S.E.

submitted to the EMBL Data Library, September 1993

A:Description: cDNA sequence of fetal rat calvarial osteoblast bone morphogenetic protein

A:Reference number: S37073

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-394 #LEN>

A:Cross-references: EMBL:Z25868; NID:q397950; PID:CAAB1088.1; PID:q397951

C:Superfamily: inhibin

## Query Match

Best Local Similarity 53.5% Score 347; DB 2; Length 394;

Matches 63; Conservative 17; Mismatches 34; Indels 2; Gaps 2;

QY 5 RQK-RPSKNIKARCSRKALHVNFKDMGWDWIITAPLEYEAFHCERGLFEPLRSHLEPTN 63

DB 279 RQAKRQRKRKSSCKRHPLYVDFSDVGNWDWIVAPGYHAFYCHGRTFPLAHILNSTN 338

QY 64 HAVIQITLMSMDPESTPTACVPTRLSPSTILFIDSANNVVKYQVDMVVEGCGCR 119

DB 439 HAVIQITLMSNVN-SKIPKACVPTLSALSMYLIDENEKVKVLKNYQDMVVEGCGCR 393

## RESULT 9

S45455

bone morphogenetic protein-2 - mouse

C:Species: Mus musculus (house mouse)

C>Date: 10-Dec-1994 #sequence\_revision 17-Nov-1995 #text\_change 03-May-1996

C:Accession: S45455

R:Refnd, J.O.: Harris, M.A.; Ghosh-Gondhury, N.; Feng, M.; Mundy, G.R.; Harris, S.E.  
Biochim. Biophys. Acta 1218, 221-224, 1994

A:Title: Structure and sequence of mouse bone morphogenetic protein-2 gene (BMP-2); c

A:Reference number: S45455; MUID:94284845

A:Accession: S45455

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-394 #LEN

C:Superfamily: inhibin

Query Match 53.5% Score 347; DB 2; Length 394;

Best Local Similarity 54.3%; Pred. No. 26-28;

Matches 63; Conservative 17; Mismatches 34; Indels 2; Gaps 2;

QY 5 RQK-RPSKNIKARCSRKALHVNFKDMGWDWIITAPLEYEAFHCERGLFEPLRSHLEPTN 63

DB 280 RQAKRQRKRKSSCKRHPLYVDFSDVGNWDWIVAPGYHAFYCHGRTFPLAHILNSTN 339

QY 64 HAVIQITLMSMDPESTPTACVPTRLSPSTILFIDSANNVVKYQVDMVVEGCGCR 119

DB 440 HAVIQITLMSNVN-SKIPKACVPTLSALSMYLIDENEKVKVLKNYQDMVVEGCGCR 394

## RESULT 10

BME02

bone morphogenetic protein 2 precursor - human

N:Alternate names: bone morphogenetic protein 2A; rhBMP2

C:Species: Homo sapiens (man)

C>Date: 16-Sep-1992 #sequence\_revision 03-Aug-1995 #text\_change 18-Jun-1999

C:Accession: B37278; PC2178

R:Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Krieger, K.W.;

Science 242, 1528-1534, 1988

A:Title: Novel regulators of bone formation: molecular clones and activities.

A:Reference number: A37278; MUID:89072730

A:Accession: B37278

A:Molecule type: mRNA

A:Residues: 1-396 #W02>

A:Cross-references: GB:M22489; NID:q179501; PID:AAA51834.1; PID:q179502

R:Shida, N.; Tsujimoto, M.; Kanaya, I.; Shimamura, A.; Tsurucka, N.; Kodama, S.; Kat

J. Biochem. 115, 279-285, 1994

A:Title: Expression and characterization of human bone morphogenetic protein-2 in sil

A:Accession: PC2178; MUID:94266754

A:Molecule type: protein

A:Residues: 290-295, X', 297-304 -LSH>

A:Experimental source: cell line BOM0-15A1ic

R:Kathore, S.; Hammerstone, K.M.; Dausorean, S.; Butler, L.J.

Protein Sci. 4(Suppl.2): 443S, 1995

A:Title: N-terminal isoforms of recombinant human bone morphogenetic protein (rhBMP-2

A:Reference number: A56729

A:Contents: annotation

A:Note: determination of amino ends of mature forms; dimers with long term chains have

C:Comment: this hormone is capable of inducing bone formation at ectopic morphological

C:Genetics:

A:Gene: GBB:BMP2A

A:Cross-references: GDB:125204; GIM:112261

A:Map position: 20p12-20p12

C:Complex: homodimer, disulfide linked

C:Superfamily: inhibin

C:Keywords: bone; dimer; glycoprotein; pyroglutamic acid

F:1-23/Domain: signal sequence #status predicted -SIG>

F:24-265/Domain: propeptide #status predicted -SIG>

F:266-396/Product: bone morphogenetic protein 2; #status predicted -MAL>

F:283-396/Product: bone morphogenetic protein 2; #status predicted -MAL>

F:145,163,164/Binding site: carboxylate (Asn) (in mature form) #status predicted -MAL>

F:283/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status exper

F:338/Binding site: carbohydrate (Asn) (covalent) #status experimental

## Query Match

Best Local Similarity 53.5% Score 347; DB 1; Length 396;

Matches 63; Conservative 17; Mismatches 34; Indels 2; Gaps 2;



Best local Similarity 48.7%; pred. No. 6,40-28;  
Matches 57; Conservative 24; Mismatches 34; Indels 2; Gaps 1;

5. 60CRR55 - KNLKARCSRAKLAHVNKDMDWOWLALVEYEAEPHCEGLCEEPFLRSHLEPT 62  
472 KHAARPTRRKHJUDTCRRHSLSVDFSDVDGOWIVAILGSDYYVHGKCFPEFLAUFENST 531  
63 NHAVIQLTMMSPGPESTPETA-VPTRLSPSLFETLSANNVVKQYEDMWVFNCR 119  
542 NHAVVQQLTANNPGRVAKACVPTQLDSVAMLYNIQGSTVWLKNVQEMIVLGRVCR 588

## 51 THUSSEN

**JH0688**  
 Bone morphogenetic protein 2II precursor - African clawed frog  
 :Species: Xenopus laevis (African clawed frog)  
 :Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Jul-1999  
 :Accession: JH0688  
 :Nucleotide: 1700bp  
 :Map: Nishimatsu, S.; Suzuki, A.; Shoda, A.; Murakami, K.; Ueno, N.  
 :Biochim. Biophys. Res. Commun. 186, 1487-1495, 1992  
 :Title: Genes for bone morphogenetic proteins are differentially transcribed in  
 :Reference number: JH0687; MIM:92378516  
 :Accession: JH0688  
 :Molecule type: mRNA  
 :Residues: 1-498 - NLS,  
 :Cross-references: CH:X63425; NID:q64583; PUN:CAA45019.1; PID:q64584  
 :Experimental source: oocyte  
 :Superfamily: Inhibin  
 :Keywords: glycoprotein  
 :DBS: 285-498/Product; bone morphogenetic protein 2II #status predicted -BATS  
 :1137, 202, 340/Binding site; carbohydrate (Asn) #status predicted

Query Match	52.9%	Score	44.3	IR	2	Length	398
Best Local Similarity	53.4%	Prod. No.	5,46-28				
Matches	62	Conservative	19	Mismatches	34	Indels	2
Gaps	2						
5	Q07K-RISKNIKARCSKHALVNFKDGMDGMDWI	LAPLEAFHACBCEGFEPLRSILEPTN	63				
	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1						
284	Q04BKQKRLKSSCRHPIYDFSDVGMDGMDWI	VAPPHYHAFYHCEGFEPLADLNSTN	343				
	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1						
64	HAVIQTLMNSDMSEPTACTCPTRISPTLFD	SANNVVYKVEFDMVVFSSNCR	119				
	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1						
444	HAIQVILVNSVN-TNIPKACQCTFELSA	SMILYDENEKVVLKNYDVMVFGCGC	498				
	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1						

Search completed: March 26, 2002, 06:09:44  
Job time: 42 sec





GenCore version 4.5  
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QW protein - protein search, using sw model

Run on: March 26, 2002, 06:09:47 ; Search time 22.3 seconds

(without alignments)

780,556 Million cell updates/sec

Title: US-09-701-121-2

Perfect score: 649

Sequence: 1 PLATROGKRP5KNIKAK\*SR.....ANNVYQVDMVVFSGCR 119

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 6%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP\_TREMBL\_17:\*  
2: SP\_Archaea:\*  
3: SP\_Bacteria:\*  
4: SP\_Fungi:\*  
5: SP\_Human:\*  
6: SP\_Invertebrate:\*  
7: SP\_Mammal:\*  
8: SP\_Misc:\*  
9: SP\_Organello:\*  
10: SP\_Phage:\*  
11: SP\_Plant:\*  
12: SP\_Rodent:\*  
13: SP\_Virus:\*  
14: SP\_Unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	637	98.2	500	13	Q9W6G0
2	587	90.4	324	13	Q9YVW9
3	563	86.7	257	13	Q42303
4	544.5	82.4	126	13	Q93573
5	527.5	81.3	261	13	Q9W6G0
6	527	81.2	413	13	Q9W6G0
7	524	80.7	399	13	Q9W6G0
8	524	80.7	412	13	Q12948
9	491	75.7	294	6	Q9BDW9
10	491	75.7	447	6	Q9BDW9
11	386	59.5	441	11	Q9MYV1
12	368.5	56.8	361	5	Q96504
13	368	56.7	204	5	Q9XZ59
14	366	56.4	411	5	Q90418
15	365	56.2	405	5	Q905B8
16	361	55.6	289	5	Q9XY08
17	359	55.4	417	5	Q9XY07
18	355.5	54.8	178	5	Q25211
19	354	54.5	67	6	Q02783

20	349.5	53.9	411	13	Q57573
21	349.5	53.9	411	13	Q93469
22	347	53.5	588	5	Q9V066
23	346	53.3	400	13	Q74818
24	346	53.3	400	13	Q91703
25	346	53.3	443	5	Q76851
26	344.5	53.1	411	13	Q14108
27	342.5	52.8	191	5	Q26468
28	342	52.7	373	13	Q90723
29	342	52.7	373	13	Q98950
30	342	52.7	400	13	Q57574
31	340	52.4	400	13	Q14107
32	338	52.1	614	5	Q91720
33	336.5	51.8	347	6	Q9M2V5
34	335	51.6	386	13	Q14109
35	335	51.6	424	13	Q9YGH7
36	334	51.5	301	5	Q97390
37	333	51.3	453	13	Q87373
38	330	50.8	177	4	Q9H512
39	330	50.8	313	13	Q91403
40	330	50.8	354	13	Q9G5V1
41	330	50.8	398	13	Q91816
42	325	50.1	432	13	Q91FF9
43	317.5	48.9	185	5	Q9G8A7
44	306.5	47.2	365	5	Q02424
45	306.5	47.2	365	5	Q76514

## ALIGNMENTS

RESULT 1  
Q9W6G0  
ID: Q9W6G0  
AC: Q9W6G0  
DT: 01-NOV-1999 (11EMBLrel. 12, created)  
DI: 01-NOV-1999 (11EMBLrel. 12, last sequence update)  
DT: 01-JUN-2001 (11EMBLrel. 17, last annotation update)  
DE: GDF-5 PROTEIN.  
GN: GDF5.  
OS: Gallus gallus (chicken).  
OC: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
NC: Archosauria; Aves; Neornithae; Galliformes; Phasianidae; Phasianinae;  
CC: Gallus.  
CX: NCBI\_LaSID: 9031;  
KW: [1]  
RP: SEQUENCE FROM N.A.  
RX: MEDLINE: 9914693; PubMed: 10021348;  
RA: Francis-West P.H., Abdellattah A., Chou P., Allen C., Parish J.,  
LA: Lohrer R., Allen S., MacPherson S., Jayden F.P., Archer C.W.;  
RT: "Mechanisms of GDF-5 action during skeletal development";  
RL: Development 126:1405-1415(1999).  
CC: 1- SIMILARITY TO THE TGF-BETA FAMILY.  
DR: EMBL: AF123389; AAB0451.1;  
DR: BSSP: P12643; 38MP.  
DR: InterPro: IPR002405; Inhibin.alpha.  
DR: InterPro: IPR001849; TGF-beta.  
DR: InterPro: IPR01111; IGFB\_N.  
DR: Pfam: PF00019; TGF-beta; 1.  
DR: Pfam: PF00688; IGFB\_propeptide; 1.  
DR: PRINTS: PK00669; INHIBINA.  
DR: ProDom: PD00357; TGF-beta; 1.  
DR: SMART: SM00204; TGF-beta; 1.  
DR: PROSITE: PS00250; TGF-BETA; 1.  
KW: Glycoprotein.  
SQ: SEQUENCE 500 AA: 55952 MW: 108385A3119A598 CR664;

Query Match: 98.2%; Score: 637; DR: 13; Length: 500;

Best Local Similarity: 97.5%; Pred. No.: 176-64;

Matches: 116; Conservative: 1; Mismatches: 2; Indels: 0; Gaps: 0;

Q9 1 PLATROGKRP5KNIKAK\*SRKALIVNEKDM3W0EW11ATPEYKAFHCTEGLTEPLKSHLE 60



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KW Glycoprotein. 1
PI NON_TER
SQ SEQUENCE 126 AA: 14265 MW: 68240280E44A394 CRC64:

Query Match
Best Local Similarity 79.08; Score 534.5; DB 13; Length 126;
Matches 94; Conservative 13; Mismatches 11; Indels 1; Gaps 1;

QY 2 LATROCKR PSKNIKARSRKALHVNPKDMGWDMWLTAPLEYEAFHCEHCEPFLRSKLE 60
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 8 LAARSGRGRCKKAKTRCSRKPLHVNFKELGWDMWLTAPLDYAYHCEGVDFPLRSKLE 67
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

QY 61 PTNHAVIQTILMNSMDPESTPTTACVPTKLSPTSLIFSDSANNVVKYQYEMVVESSGR 119
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 68 PTNHAIQTILMNSMDPESTPTSCVPSKLSPTSLIFSDSNNVVVKYQYEMVVESSGR 126
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

RESULT 5
QW6630
AC QW6630 PRELIMINARY: PRI: 261 AA.
DT 01-NOV-1999 (FEMBLrel. 12, Created)
DI 01-NOV-1999 (FEMBLrel. 12, Last sequence update)
DE 01-JUN-2001 (FEMBLrel. 17, Last annotation update)
DE GROWTH/DIFFERENTIATION FACTOR 7 (FRAGMENT).
GN GDF7.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID: 7955;
RN 111
RP SEQUENCE FROM N.A.
RX MEDLINE 99148135; PubMed 16022976;
RA Davidson A.J., Postlethwait J.H., Yan Y.L., Beier D.R., van Doren C.,
RA Everszler D., Celeste A.J., Grosier K.E., Grosier P.S.;
RT "Isolation of zebrafish gdf7 and comparative genetic mapping of clones
RT belonging to the growth/differentiation factor 5, 6, 7 subgroup of the
RT TGF-beta superfamily."
RL Genome Res. 9:121-129(1999).
CC -1- SIMILARITY: TO THE TGF-BETA FAMILY.
DR EMBL: AF113023; AAC20829.1; -.
DR HSSP: P12643; 48MP.
DR InterPro: IPR002400; GF_cysknot.
DR InterPro: IPR002405; Inhibin_alpha.
DR InterPro: IPR01839; TGF-beta.
DR Pfam: PF00019; TGF-beta; 1.
DR PRINTS: PR00438; GFYSKNT.
DR PRINTS: PR00669; INHIBINA.
DR ProDom: PD000457; TGF-beta; 1.
DR SMART: SM00204; TGF-beta; 1.
DR PROSITE: PS00250; TGF-BETA; 1.
KW Glycoprotein. 1
PI NON_TER
SQ SEQUENCE 261 AA: 29414 MW: 773456977045A104 CRC64:

Query Match
Best Local Similarity 81.48; Score 527.5; DB 13; Length 261;
Matches 95; Conservative 11; Mismatches 12; Indels 7; Gaps 1;

QY 2 LATROCKRPSKNIKARSRKALHVNFKDMGWDMWLTAPLEYEAFHCEHCEPFLRSKLE 54
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 147 LAGRGVGVPTSGGKGGRRRTCSRKPLHVNFKELGWDMWLTAPLDYAYHCEGVDFPLRSKLE 196
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

QY 55 LRSHPLEPTNHAVIQTILMNSMDPESTPTTACVPTKLSPTSLIFSDSANNVVKYQYEMVVE 114
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 147 LRSHPLEPTNHAIQTILMNSMDPESTPTSCVPSKLSPTSLIFSDSNNVVVKYQYEMVVE 256
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

QY 115 SSGGR 119
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 257 SSGGR 261
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

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RESULT 6
QW63N4
AC QW63N4 PRELIMINARY: PRI: 413 AA.
DT 01-MAR-2001 (FEMBLrel. 16, Created)
DI 01-MAR-2001 (FEMBLrel. 16, Last sequence update)
DE 01-JUN-2001 (FEMBLrel. 17, Last annotation update)
DE GROWTH/DIFFERENTIATION FACTOR 16 PRECURSOR PROTEIN.
GN GDF16.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID: 8455;
RN 111
RP SEQUENCE FROM N.A.
RX PubMed 10906478;
RA Vokes S.A., Kried P.A.;
RT "Gdf16, a novel member of the growth/differentiation factor subgroup
RT of the TGF-beta superfamily, is expressed in the hindbrain and
RT epibranchial placodes."
RL Mech. Dev. 95:279-283(2000).
CC -1- SIMILARITY: TO THE TGF-BETA FAMILY.
DR EMBL: AF25976; AAF99597.1; -.
DR InterPro: IPR001839; TGF-beta.
DR InterPro: IPR001111; TGF-beta.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGF-beta; 1.
DR ProDom: PD000457; TGF-beta; 1.
DR SMART: SM00204; TGF-beta; 1.
DR PROSITE: PS00250; TGF-BETA; 1.
KW Glycoprotein; Signal 24.
PI POTENTIAL.
FT SIGNAL 1
SQ SEQUENCE 413 AA: 46510 MW: 516007097E591F6 CRC64:

Query Match
Best Local Similarity 81.2%; Score 527; DB 13; Length 413;
Matches 92; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

QY 1 PLATROCKRPSKNIKARSRKALHVNFKDMGWDMWLTAPLEYEAFHCEHCEPFLRSKLE 60
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 295 PTINCKGKHAHAKSRKSKKPLHVNFKELGWDMWLTAPLDYAYHCEGVDFPLRSKLE 454
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

QY 61 PTNHAVIQTILMNSMDPESTPTTACVPTKLSPTSLIFSDSANNVVKYQYEMVVESSGR 119
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 455 PTNHAIQTILMNSMDPESTPTSCVPSKLSPTSLIFSDSNNVVVKYQYEMVVESSGR 414
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

RESULT 7
QW754
AC QW754 PRELIMINARY: PRI: 499 AA.
DT 01-NOV-1999 (FEMBLrel. 12, Created)
DI 01-NOV-1999 (FEMBLrel. 12, Last sequence update)
DE 01-JUN-2001 (FEMBLrel. 17, Last annotation update)
DE GROWTH AND DIFFERENTIATION FACTOR 6.
GN GDF6.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID: 8455;
RN 111
RP SEQUENCE FROM N.A.
RX Chang C., Brattini-Brianou A.;
RT "Xenopus GDF6, a new antagonist of noggin and a partner of BMPs."
RL Development 120:9(1999).
CC -1- SIMILARITY: TO THE TGF-BETA FAMILY.
DR EMBL: AF155125; AAD38402.1; -.
DR HSSP: P12643; 48MP.

```













GenCore version 4.5  
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0M protein - protein search, using sw model

Run on: March 26, 2002, 06:09:27 : Search time 11.67 seconds  
(without alignments)  
373,874 Million cell updates/sec

Title: US-09-701-121-2

Perfect score: 649  
Sequence: 1 PLATROCKKSKNIKARCSR.....ANNVYKQYEDMVVSEVGR 119

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 46664827 residues  
Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_49.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	640	98.6	495	1 GDF5_MOUSE	P43027 mus musculus
2	639	98.5	501	1 GDF5_HUMAN	P43026 homo sapien
3	543	84.7	125	1 GDF6_MOUSE	P43028 mus musculus
4	528	81.4	436	1 GDF6_BOVIN	P55106 bos taurus
5	493	76.0	151	1 GDF7_MOUSE	P43029 mus musculus
6	454.5	54.5	461	1 DVL1_STRPO	P48969 strongyloce
7	452	54.2	395	1 UNIV_STRPO	P48970 strongyloce
8	447	53.5	393	1 BMP2_RAT	P14901 rattus norv
9	447	53.5	394	1 BMP2_MOUSE	P21274 mus musculus
10	447	53.5	395	1 BMP2_RABIT	P46564 oncotolagus
11	447	53.5	396	1 BMP2_DAMIA	U19006 dama dama
12	447	53.5	396	1 BMP2_HUMAN	P12643 homo sapien
13	447	53.5	401	1 BMP4_XENLA	P40885 xenopus lae
14	447	53.5	594	1 DECA_DROSI	P91706 drosophila
15	446	53.3	405	1 BMP4_CHICK	Q90752 gallus gall
16	444	53.0	588	1 DECA_DROME	P07713 drosophila
17	443	52.9	398	1 BMP4_XENLA	P25703 xenopus lae
18	443	52.9	398	1 BMP8_XENLA	P40884 xenopus lae
19	441	52.5	408	1 BMP4_MOUSE	P1275 mus musculus
20	441	52.5	408	1 BMP4_RAT	Q06826 rattus norv
21	439	52.2	408	1 BMP4_HUMAN	P12644 homo sapien
22	438	52.1	372	1 DECA_TRIICA	Q26974 trikolium c
23	438	52.1	408	1 BMP4_DAMIA	Q26907 dama dama
24	437	51.9	353	1 BMP2_CHICK	Q90751 gallus gall
25	436	51.8	409	1 BMP4_RABIT	Q46576 oncotolagus
26	435	51.6	355	1 DVL1_HHARE	P45621 brachydanio
27	434	51.5	621	1 DECA_DROPS	P91699 drosophila
28	433	51.4	207	1 BMP6_RAT	Q94906 rattus norv
29	433	51.4	452	1 BMP5_MOUSE	P49003 mus musculus
30	433	51.4	454	1 BMP5_HUMAN	P22003 homo sapien
31	432	51.2	513	1 BMP6_HUMAN	P22004 homo sapien
32	430	50.8	431	1 BMP7_HUMAN	P18075 homo sapien
33	429	50.7	510	1 BMP6_MOUSE	P20722 mus musculus

## ALIGNMENTS

RESULT 1	ID	GDF5_MOUSE	STANDARD	PRU	495 AA
AC	P43027				
DI	01-NOV-1995	(Rel. 42, Created)			
DI	01-NOV-1995	(Rel. 42, Last sequence update)			
DI	20-AUG-2001	(Rel. 40, Last annotation update)			
DE	GROWTH/DIFFERENTIATION FACTOR 5 PRECURSOR (GDF-5).				
GN	GDF5 OR GDF-5 OR DF.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Plathia; Rodentia; Sciurognathi; Muridae; Mus.				
OX	NCBI_TaxID 10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN Cl-1; TISSUE Embryo;				
RX	MEDLINE:94195427; PubMed:8145850;				
RA	Storm E.E., Hayth T.V., Copeland N.G., Jenkins N.A., Kinsey D.M.,				
RA	Lee S.-J.;				
RI	*Limb alterations in brachypodism mice due to mutations in a new				
RT	member of the TGF-beta superfamily.";				
RL	Nature 368:639-643(1994).				
CC	-1- FUNCTION: COULD BE INVOLVED IN BONE FORMATION.				
CC	-1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).				
CC	-1- DISEASE: DEFECTS IN GDF-5 ARE THE CAUSE OF BRAHYPODISM WHICH				
CC	ALTERS THE LENGTH AND NUMBERS OF BONES IN THE LIMBS BUT SPARES THE				
CC	AXIAL SKELETON.				
CC	-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.				
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	the European Bioinformatics Institute. There are no restrictions on its				
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).				
CC	EMBL: 008347; AAA18778.1; -				
DR	BSSP; P18075; 1BMP.				
DR	MGD; MGI:95688; Gdf5.				
DR	InterPro: IPR002400; GF_cysknott.				
DR	InterPro: IPR001849; TGF-beta.				
DR	InterPro: IPR001111; TGFb_N.				
DR	Pfam: PF00019; TGF beta; 1.				
DR	Pfam: PF00688; TGFb_propeptide; 1.				
DR	PRINTS: PR00438; GDFYSKNKT.				
DR	ProDom: PD000457; TGF-beta; 1.				
DR	SMART: SM00204; IGFB; 1.				
DR	PROSITE: PS00250; TGF_BETA_1; 1.				
KW	Signal; Growth factor; Cytokine; Glycoprotein; Polymorphism.				
FT	SIGNAL 1 27 POTENTIAL.				
FT	PROPEP 28 375 POTENTIAL.				
FT	CHAIN 376 495 GROWTH/DIFFERENTIATION FACTOR 5.				
FT	DISULFID 494 466 BY SIMILARITY.				
FT	DISULFID 423 492 BY SIMILARITY.				
FT	DISULFID 427 494 BY SIMILARITY.				

P40886 xenopus lae  
P24459 mus musculus  
P44820 homo sapien  
P44821 mus musculus  
P09544 xenopus lae  
P27091 drosophila  
Q24735 gallus gall  
Q95993 drosophila  
Q91229 homo sapien  
Q99556 mus musculus  
Q99123 homo sapien

FT DISULFID 459 459 INTERCHAIN (BY SIMILARITY).  
 FT CARRIER 183 183 N LINKED (GLYNAV... ) (POTENTIAL).  
 FT VARIANT 98 98 S...P.  
 SQ SEQUENCE 495 AA; 54885 MW; CD005DE481892E3 C6664;  
 Query Match  
 Best Local Similarity 98.68; Score 640; DB 1; Length 495;  
 Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 PLATROCKRKSNNKAKCSKALVNFKMGWIDWIAIYEFAPRFGH/CTFFPSHLE 60  
 DB 477 PLATROCKRKSNNKAKCSKALVNFKMGWIDWIAIYEFAPRFGH/CTFFPSHLE 446  
 QY 61 PINHAVIQTILNMSMDPSTPTACVTRISPTSLIFUSANNVVKYEDMVVVSQGR 119  
 DB 437 PINHAVIQTILNMSMDPSTPTACVTRISPTSLIFUSANNVVKYEDMVVVSQGR 495  
 RESULT 2  
 ID GDF5 HUMAN STANDARD; PRI; 501 AA.  
 AC P44026;  
 DT 01-NOV-1995 (Ref. 42, Created)  
 DI 01-FEB-1996 (Ref. 43, Last sequence update)  
 DI 20-AUG-2001 (Ref. 40, Last annotation update)  
 DE GROWTH/DIFFERENTIATION FACTOR 5 PRECURSOR (GDF-5) (CARTILAGE-DERIVED  
 DE MORPHOGENETIC PROTEIN 1) (CMBP 1).  
 GN GDF5 OR CMBP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID 9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE Placenta;  
 RX MEDLINE 95050604; PubMed 7989526;  
 RA Chang S., Beard B., Thomas J.T., Vukicevic S., Layton E.P.,  
 RA Kyba N.J.P., Kozak C.A., Roddi A.H., Mees M.;  
 RT "Cartilage-derived morphogenetic proteins. New members of the  
 RT transforming growth factor beta superfamily predominantly expressed  
 RT in long bones during human embryonic development.";  
 RL J. Biol. Chem. 269:28227-28234(1994).  
 CC 1- FUNCTION: SHOULD BE INVOLVED IN BONE FORMATION.  
 CC 1- SUBUNIT: DIMER; DISULFIDE-LINKED (BY SIMILARITY).  
 CC 1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN LONG BONES DURING  
 CC HUMAN EMBRYONIC DEVELOPMENT.  
 CC 1- DISEASE: DEFECTS IN GDF5 ARE A CAUSE OF ACHROPLASIA  
 CC CHONDRODYSPLASIA OF THE HUNTER-THOMPSON TYPE. THIS FORM OF  
 CC DWARFISM IS CHARACTERIZED BY SHORT FOREARMS, HANDS AND FEET. THE  
 CC RADIUS IS CURVED AND ITS HEAD IS OFTEN DISLOCATED POSTEROLATERALLY. THE  
 CC METACARPALS, METATARSALS AND PHALANGES ARE PARTICULARLY SHORT. THE  
 CC PHALANGES ARE ALMOST SQUARE.  
 CC 1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 CC  
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 CC THE EUROPEAN BIOINFORMATICS INSTITUTE. THERE ARE NO RESTRICTIONS ON ITS  
 CC USE BY NON-PROFIT INSTITUTIONS AS LONG AS ITS CONTENT IS IN NO WAY  
 CC MODIFIED AND THIS STATEMENT IS NOT REMOVED. USAGE BY AND FOR COMMERCIAL  
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 CC or send an email to [license@sib.ch](mailto:license@sib.ch)).  
 DR EMBL; X55915; CAA56874.1;  
 DR EMBL; 010660; AAA57007.1;

DR ISSY; PIR075; IIRP;  
 DR MIM; 601136;  
 DR MIM; 261250;  
 DR MIM; 200700;  
 DR InterPro: IPR002400; GDF cysteine.  
 DR InterPro: IPR001849; TGF-beta.  
 DR InterPro: IPR001111; TGF-beta.  
 DR Pfam: PF00019; TGF-beta; 1.  
 DR Pfam: PF00688; TGF-beta; 1.  
 DR Pfam: PF00408; GDF cysteine.  
 DR ProDom: PD00045; TGF-beta; 1.  
 DR SMART: SM00204; TGF-beta; 1.  
 DR PROSITE: PS00250; TGF-beta; 1.  
 KW Signal; Growth factor; Cytokine; Glycoprotein.  
 FT SIGNAL 1 27  
 FT PROPEP 28 481  
 FT CHAIN 482 501  
 FT DISULFID 400 466  
 FT DISULFID 429 498  
 FT DISULFID 433 500  
 FT DISULFID 465 465  
 FT CARBOHYD 189 189  
 FT CONFLICT 38 38  
 FT CONFLICT 254 258  
 FT CONFLICT 276 276  
 FT CONFLICT 321 321  
 FT CONFLICT 484 484  
 SQ SEQUENCE 501 AA; 55640 MW; EEF63DA041A448 C6664;  
 Query Match  
 Best Local Similarity 98.49; Score 639; DB 1; Length 501;  
 Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 PLATROCKRKSNNKAKCSKALVNFKMGWIDWIAIYEFAPRFGH/CTFFPSHLE 60  
 DB 483 PLATROCKRKSNNKAKCSKALVNFKMGWIDWIAIYEFAPRFGH/CTFFPSHLE 442  
 QY 61 PINHAVIQTILNMSMDPSTPTACVTRISPTSLIFUSANNVVKYEDMVVVSQGR 119  
 DB 443 PINHAVIQTILNMSMDPSTPTACVTRISPTSLIFUSANNVVKYEDMVVVSQGR 501  
 RESULT 3  
 ID GDF6 MOUSE STANDARD; PRI; 125 AA.  
 AC P44028;  
 DT 01-NOV-1995 (Ref. 42, Created)  
 DI 01-NOV-1995 (Ref. 42, Last sequence update)  
 DI 20-AUG-2001 (Ref. 40, Last annotation update)  
 DE GROWTH/DIFFERENTIATION FACTOR 6 PRECURSOR (GDF-6) (PDA-MENT).  
 GN GDF6 OR GDF-6.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID 10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN BALB/c; TISSUE Liver;  
 RX MEDLINE 9419427; PubMed 9449650;  
 RA Storm E.E., Hryb L.V., Copeland N.G., Jenkins N.A., Kingsley D.M.,  
 RA Lee S.J.;  
 RI "Limb alterations in brachypodism arise due to mutations in a new  
 RI member of the TGF-beta superfamily.";  
 RL Nature 381:649-653(1994).  
 CC 1- SUBUNIT: DIMER; DISULFIDE-LINKED (BY SIMILARITY).  
 CC 1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 CC  
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 DR EMBL; X55915; CAA56874.1;  
 DR EMBL; 010660; AAA57007.1;

















